

IAP9 Rec'd PCT/PTO 05 SEP 2006

1/22

SEQUENCE LISTING

<110> Japan Science and Technology Corporation

<120> Epilepsy-model animal

<130> 05F004PCT

<140> PCT/JP2005/003430

<141> 2005-03-05

<150> JP2004-62907

<151> 2004-03-05

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 627

<212> PRT

<213> Homo sapiens

<400> 1

Met Glu Leu Gly Gly Pro Gly Ala Pro Arg Leu Leu Pro Pro Leu Leu
1 5 10 15

Leu Leu Leu Gly Thr Gly Leu Leu Arg Ala Ser Ser His Val Glu Thr
20 25 30

Arg Ala His Ala Glu Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr
35 40 45

Asn Lys Trp Ser Arg Pro Val Ala Asn Ile Ser Asp Val Val Leu Val
50 55 60

Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn
65 70 75 80

BEST AVAILABLE COPY

2/22

Gln Met Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr
85 90 95

Lys Leu Arg Trp Asp Pro Ala Asp Tyr Glu Asn Val Thr Ser Ile Arg
100 105 110

Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn
115 120 125

Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His Leu Phe
130 135 140

His Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys Ser Ser
145 150 155 160

Cys Ser Ile Asp Val Thr Phe Phe Pro Asp Gln Gln Asn Cys Thr
165 170 175

Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val
180 185 190

Asn Met His Ser Arg Val Asp Gln Leu Asp Phe Trp Glu Ser Gly Glu
195 200 205

Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys Tyr Glu
210 215 220

Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Phe Val Ile Arg
225 230 235 240

Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu
245 250 255

Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly

3/22

260

265

270

Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe
275 280 285

Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro
290 295 300

Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser
305 310 315 320

Ile Val Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg
325 330 335

Thr His Thr Met Pro Thr Trp Val Arg Arg Val Phe Leu Asp Ile Val
340 345 350

Pro Arg Leu Leu Leu Met Lys Arg Pro Ser Val Val Lys Asp Asn Cys
355 360 365

Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Ser Ala Pro Arg Phe
370 375 380

Trp Pro Glu Pro Glu Gly Glu Pro Pro Ala Thr Ser Gly Thr Gln Ser
385 390 395 400

Leu His Pro Pro Ser Pro Ser Phe Cys Val Pro Leu Asp Val Pro Ala
405 410 415

Glu Pro Gly Pro Ser Cys Lys Ser Pro Ser Asp Gln Leu Pro Pro Gln
420 425 430

Gln Pro Leu Glu Ala Glu Lys Ala Ser Pro His Pro Ser Pro Gly Pro
435 440 445

4/22

Cys Arg Pro Pro His Gly Thr Gln Ala Pro Gly Leu Ala Lys Ala Arg
450 455 460

Ser Leu Ser Val Gln His Met Ser Ser Pro Gly Glu Ala Val Glu Gly
465 470 475 480

Gly Val Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Pro Arg Asp
485 490 495

Asp Ala Ala Pro Glu Ala Asp Gly Gln Ala Ala Gly Ala Leu Ala Ser
500 505 510

Arg Asn Thr His Ser Ala Glu Leu Pro Pro Pro Asp Gln Pro Ser Pro
515 520 525

Cys Lys Cys Thr Cys Lys Lys Glu Pro Ser Ser Val Ser Pro Ser Ala
530 535 540

Thr Val Lys Thr Arg Ser Thr Lys Ala Pro Pro Pro His Leu Pro Leu
545 550 555 560

Ser Pro Ala Leu Thr Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp
565 570 575

His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys
580 585 590

Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile
595 600 605

Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala
610 615 620

5/22

Gly Met Ile
625

<210> 2
<211> 2149
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (10)..(1902)
<223>

<300>
<308> GenBank/NM_024354
<309> 2003-12-21

<400> 2
 agcttcacc atg gcc aat tcg ggc ccc ggg gcg ccg ccg ctg ctg cta 51
 Met Ala Asn Ser Gly Pro Gly Ala Pro Pro Pro Leu Leu Leu
 1 5 10

ctg ccg ctg ctg ctc cta ggg acc ggc ctc ttg cct gct agc agc 99
 Leu Pro Leu Leu Leu Leu Gly Thr Gly Leu Leu Pro Ala Ser Ser
 15 20 25 30

cac ata gag acc cgg gcc cat gcg gag cgg ctc ctg aag aga ctc 147
 His Ile Glu Thr Arg Ala His Ala Glu Glu Arg Leu Leu Lys Arg Leu
 35 40 45

ttc tcc ggt tac aac aag tgg tct cgg cca gta ggc aat atc tca gat 195
 Phe Ser Gly Tyr Asn Lys Trp Ser Arg Pro Val Gly Asn Ile Ser Asp
 50 55 60

gtg gtc ctc gtc cgc ttt ggc ttg tcc att gct cag ctc att gac gtg 243
 Val Val Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val
 65 70 75

gac gag aag aac cag atg atg aca acc aac gtg tgg gtg aag cag gag 291
 Asp Glu Lys Asn Gln Met Met Thr Thr Asn Val Trp Val Lys Gln Glu
 80 85 90

tgg cac gac tac aag ctg cgc tgg gac cct ggt gac tac gag aat gtc 339

6/22

Trp His Asp Tyr Lys Leu Arg Trp Asp Pro Gly Asp Tyr Glu Asn Val			
95	100	105	110
acc tcc atc cgc atc ccc tct gaa ctc atc tgg agg cct gac atc gtc			387
Thr Ser Ile Arg Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp Ile Val			
115	120	125	
ctc tac aac aat gcg gat gga gac ttt gca gtc acc cac ctg acc aag			435
Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys			
130	135	140	
gcc cac ctg ttc tat gac gga agg gtg cag tgg aca ccc cca gcc atc			483
Ala His Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile			
145	150	155	
tat aag agc tcc tgc agc atc gac gtc acc ttc ttc ccc ttt gac cag			531
Tyr Lys Ser Ser Cys Ser Ile Asp Val Thr Phe Phe Pro Phe Asp Gln			
160	165	170	
cag aac tgt acc atg aag ttt gga tcc tgg acc tac gac aag gcc aag			579
Gln Asn Cys Thr Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys			
175	180	185	190
att gac tta gtg agc att cat agc cgt gtg gac caa ctg gac ttc tgg			627
Ile Asp Leu Val Ser Ile His Ser Arg Val Asp Gln Leu Asp Phe Trp			
195	200	205	
gaa agt egg gag tgg gtc atc gtg gat gct gtg ggc acc tac aac acc			675
Glu Ser Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr			
210	215	220	
agg aag tac gag tgc tgt gcc gag atc tat cct gac atc acc tat gcc			723
Arg Lys Tyr Glu Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala			
225	230	235	
ttc atc atc cga cgc ctg ccg cta ttc tac acc atc aac ctc atc atc			771
Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile			
240	245	250	
ccg tgc ctg ctc atc tcc tgt ctc acc gtg ctg gtc ttc tat ctg cct			819
Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro			
255	260	265	270
tca gag tgt ggc gag aag gtc aca ctg tgc atc tcg gtg ctg ctt tct			867
Ser Glu Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu Leu Ser			

7/22

275	280	285	
ctc acc gtc ttc ctg ctg ctc atc acc gag atc atc ccg tcc acc tcg Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser			915
290	295	300	
ctg gtc atc ccg ctc atc ggc gag tac ctc ctc ttc acc atg atc ttc Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe			963
305	310	315	
gtc acc ctc tcc atc gtc atc acg gtc ttc gtg ctc aat gtg cac cac Val Thr Leu Ser Ile Val Ile Thr Val Phe Val Leu Asn Val His His			1011
320	325	330	
cgc tcg cca cgc aca cac acg atg ccc gcc tgg gtg cgt aga gtc ttc Arg Ser Pro Arg Thr His Thr Met Pro Ala Trp Val Arg Arg Val Phe			1059
335	340	345	350
ctg gac atc gtg cct cgc ctc ctc ttc atg aag cgc ccc tct gtg gtc Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Val Val			1107
355	360	365	
aaa gac aac tgc cgg aga ctt att gag tcc atg cac aag atg gcc aac Lys Asp Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn			1155
370	375	380	
gcc ccc cgc ttc tgg cca gag cct gtg ggc gag ccc ggc atc ttg agt Ala Pro Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser			1203
385	390	395	
gac atc tgc aac caa ggt ctg tca cct gcc cca act ttc tgc aac ccc Asp Ile Cys Asn Gln Gly Leu Ser Pro Ala Pro Thr Phe Cys Asn Pro			1251
400	405	410	
acg gac aca gca gtc gag acc cag cct acg tgc agg tca ccc ccc ctt Thr Asp Thr Ala Val Glu Thr Gln Pro Thr Cys Arg Ser Pro Pro Leu			1299
415	420	425	430
gag gtc cct gac ttg aag aca tca gag gtt gag aag gcc agt ccc tgt Glu Val Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala Ser Pro Cys			1347
435	440	445	
cca tcg cct ggc tcc tgt cct cca ccc aag acg acg agt ggg gct cca Pro Ser Pro Gly Ser Cys Pro Pro Pro Lys Ser Ser Ser Gly Ala Pro			1395
450	455	460	

8/22

atg ctc atc aaa gcc agg tcc ctg agt gtc cag cat gtg ccc agc tcc Met Leu Ile Lys Ala Arg Ser Leu Ser Val Gln His Val Pro Ser Ser 465 470 475	1443
caa gaa gca gca gaa gat ggc atc cgc tgc cgg tct cgg agt atc cag Gln Glu Ala Ala Glu Asp Gly Ile Arg Cys Arg Ser Arg Ser Ile Gln 480 485 490	1491
tac tgt gtt tcc caa gat gga gct gcc tcc ctg gct gac agc aag ccc Tyr Cys Val Ser Gln Asp Gly Ala Ala Ser Leu Ala Asp Ser Lys Pro 495 500 505 510	1539
acc agc tcc ccg acc tcc ctg aag gcc cgt cca tcc cag ctt ccc gtg Thr Ser Ser Pro Thr Ser Leu Lys Ala Arg Pro Ser Gln Leu Pro Val 515 520 525	1587
tca gac cag gcc tct cca tgc aaa tgc aca tgc aag gaa cca tct cct Ser Asp Gln Ala Ser Pro Cys Lys Cys Thr Cys Lys Glu Pro Ser Pro 530 535 540	1635
gtg tcc cca gtc act gtg ctc aag gcg gga ggc acc aaa gca cct ccc Val Ser Pro Val Thr Val Leu Lys Ala Gly Gly Thr Lys Ala Pro Pro 545 550 555	1683
caa cac ctg ccc ctg tca cca gcc ctg aca cgg gca gta gaa ggc gtc Gln His Leu Pro Leu Ser Pro Ala Leu Thr Arg Ala Val Glu Gly Val 560 565 570	1731
cag tac att gca gac cac ctc aag gca gaa gac act gac ttc tcg gtg Gln Tyr Ile Ala Asp His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val 575 580 585 590	1779
aag gag gac tgg aaa tac gtg gcc atg gtc att gac cga atc ttc ctc Lys Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu 595 600 605	1827
tgg atg ttc atc att gtc tgc ctt ctg ggc act gtg gga ctc ttc ctg Trp Met Phe Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu 610 615 620	1875
cct ccc tgg ctg gct ggt atg atc tag ggacgtggtg gtgcccagct Pro Pro Trp Leu Ala Gly Met Ile 625 630	1922

9/22

cccacatctc tggtagggcca tacgactcggt cagtcacccca catcttccaa accggctgac	1982
catgagacac ccttaggagag agatgtatgct tcttggggaga tggaagtgg ccctggttct	2042
agtcaagacta tgggcgtgggt tggagagaaa tgagggctga tacagttgca ggcccgagtcc	2102
ccattaaagt ttctccagag caagtggcag tactccctga cttagcag	2149

<210> 3
 <211> 630
 <212> PRT
 <213> Rattus norvegicus
 <400> 3

Met Ala Asn Ser Gly Pro Gly Ala Pro Pro Pro Leu Leu Leu Leu Pro			
1	5	10	15

Leu Leu Leu Leu Leu Gly Thr Gly Leu Leu Pro Ala Ser Ser His Ile		
20	25	30

Glu Thr Arg Ala His Ala Glu Glu Arg Leu Leu Lys Arg Leu Phe Ser		
35	40	45

Gly Tyr Asn Lys Trp Ser Arg Pro Val Gly Asn Ile Ser Asp Val Val		
50	55	60

Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu			
65	70	75	80

Lys Asn Gln Met Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His		
85	90	95

Asp Tyr Lys Leu Arg Trp Asp Pro Gly Asp Tyr Glu Asn Val Thr Ser		
100	105	110

Ile Arg Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp Ile Val Leu Tyr

10/22

115

120

125

Asn Asn Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His
 130 135 140

Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys
 145 150 155 160

Ser Ser Cys Ser Ile Asp Val Thr Phe Phe Pro Asp Gln Gln Asn
 165 170 175

Cys Thr Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys Ile Asp
 180 185 190

Leu Val Ser Ile His Ser Arg Val Asp Gln Leu Asp Phe Trp Glu Ser
 195 200 205

Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys
 210 215 220

Tyr Glu Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Phe Ile
 225 230 235 240

Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys
 245 250 255

Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Glu
 260 265 270

Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr
 275 280 285

Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val
 290 295 300

11/22

Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr
305 310 315 320

Leu Ser Ile Val Ile Thr Val Phe Val Leu Asn Val His His Arg Ser
325 330 335

Pro Arg Thr His Thr Met Pro Ala Trp Val Arg Arg Val Phe Leu Asp
340 345 350

Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Val Val Lys Asp
355 360 365

Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala Pro
370 375 380

Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser Asp Ile
385 390 395 400

Cys Asn Gln Gly Leu Ser Pro Ala Pro Thr Phe Cys Asn Pro Thr Asp
405 410 415

Thr Ala Val Glu Thr Gln Pro Thr Cys Arg Ser Pro Pro Leu Glu Val
420 425 430

Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala Ser Pro Cys Pro Ser
435 440 445

Pro Gly Ser Cys Pro Pro Pro Lys Ser Ser Ser Gly Ala Pro Met Leu
450 455 460

Ile Lys Ala Arg Ser Leu Ser Val Gln His Val Pro Ser Ser Gln Glu
465 470 475 480

12/22

Ala Ala Glu Asp Gly Ile Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys
485 490 495

Val Ser Gln Asp Gly Ala Ala Ser Leu Ala Asp Ser Lys Pro Thr Ser
500 505 510

Ser Pro Thr Ser Leu Lys Ala Arg Pro Ser Gln Leu Pro Val Ser Asp
515 520 525

Gln Ala Ser Pro Cys Lys Cys Thr Cys Lys Glu Pro Ser Pro Val Ser
530 535 540

Pro Val Thr Val Leu Lys Ala Gly Gly Thr Lys Ala Pro Pro Gln His
545 550 555 560

Leu Pro Leu Ser Pro Ala Leu Thr Arg Ala Val Glu Gly Val Gln Tyr
565 570 575

Ile Ala Asp His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu
580 585 590

Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met
595 600 605

Phe Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro Pro
610 615 620

Trp Leu Ala Gly Met Ile
625 630

<210> 4

<211> 4508

<212> DNA

13/22

<213> Mus musculus

<220>

<221> CDS

<222> (105).. (1994)

<223>

<300>

<308> GenBank/NM_015730

<309> 2003-12-23

<400> 4

cgagcggccg cgacacgggg catgaagtgc ggtgcgcgcg ggtctcgag cggaggcg 60

gtactgccgg gagccgcctt cgictagagc ccgttctgtg agcc atg gag atc ggg 116
Met Glu Ile Gly
1ggc tcc ggg gcg ccg ccg ctg ctg ctc ctg ccg ctc ctg ctg ctc 164
Gly Ser Gly Ala Pro Pro Leu Leu Leu Pro Leu Leu Leu Leu
5 10 15 20ttt ggg acc ggc ctc ttg cct gct agc agc cac ata gag acc ccg gcc 212
Leu Gly Thr Gly Leu Leu Pro Ala Ser Ser His Ile Glu Thr Arg Ala
25 30 35cat gcg gag gag cgg ctc ctg aag aga ctc ttc tct ggc tac aac aag 260
His Ala Glu Glu Arg Leu Leu Lys Arg Leu Phe Ser Gly Tyr Asn Lys
40 45 50tgg tct cgg cca gta gcc aat atc tca gat gtg gtc ctt gtc cgc ttt 308
Trp Ser Arg Pro Val Ala Asn Ile Ser Asp Val Val Leu Val Arg Phe
55 60 65ggc ttg tcg att gct cag ctc att gat gtg gat gag aaa aac cag atg 356
Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met
70 75 80atg acg acc aac gtg tgg aag cag gag tgg cat gac tac aaa ctg 404
Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu
85 90 95 100cgc tgg gac cct ggt gac tac gag aat gtc acc tcc atc cgc atc cca 452
Arg Trp Asp Pro Gly Asp Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro
105 110 115

14/22

tct gaa ctc atc tgg agg cct gac atc gtc ctc tac aac aac gcg gac		500	
Ser Glu Leu Ile Trp Arg Pro Asp Ile Val Leu Tyr Asn Asn Ala Asp			
120	125	130	
ggg gac ttt gca gtc acc cac cta acc aaa gcc cac ctg ttc tat gat		548	
Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His Leu Phe Tyr Asp			
135	140	145	
ggg cgt gtg cag tgg aca ccc ccg gcc atc tat aag agc tcc tgc agc		596	
Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser			
150	155	160	
atc gac gtc acc ttc ttc ccc ttc gac cag cag aac tgt acc atg aag		644	
Ile Asp Val Thr Phe Phe Pro Asp Gln Gln Asn Cys Thr Met Lys			
165	170	175	180
ttt ggg tcc tgg acc tac gac aag gcc aag att gac ttg gtg agc atg		692	
Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Met			
185	190	195	
cac agc cgt gtg gac caa ctg gac ttc tgg gaa agt ggg gag tgg gtc		740	
His Ser Arg Val Asp Gln Leu Asp Phe Trp Glu Ser Gly Glu Trp Val			
200	205	210	
att gtg gat gcc gtg ggc acc tac aac acc agg aag tat gaa tgc tgt		788	
Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys Tyr Glu Cys Cys			
215	220	225	
gcc gag atc tat cct gac atc acc tac gcc ttc atc atc cgc cga ctg		836	
Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Phe Ile Ile Arg Arg Leu			
230	235	240	
cca ctg ttc tac acc atc aac ctt atc atc ccg tgc ctg ctc atc tcc		884	
Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser			
245	250	255	260
tgc ctc acc gtg ctg gtc ttc tat ctg ccc tgc gag tgc ggc gag aag		932	
Cys Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys			
265	270	275	
gtc acg ctg tgc atc tcg gtg ctg ctt tct ctc acc gtc ttc ctg ctg		980	
Val Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu			
280	285	290	

15/22

ctc atc acc gag atc atc ccg tcc acc tcg ctg gtc atc ccg ctc atc Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile 295 300 305	1028
ggc gag tac ctg ctc ttc acc atg atc ttc gtc acc ctc tcc att gtc Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val 310 315 320	1076
atc acg gtc ttc gtg ctc aat gta cac cac cgc tca cca cgc aca cac Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His 325 330 335 340	1124
acc atg ccc gcc tgg gtg cgc aga gtc ttc ctg gac att gtg ccc cgt Thr Met Pro Ala Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg 345 350 355	1172
ctc ctc ttc atg aag cgc cca tct gtg gtc aaa gac aac tgc cgg aga Leu Leu Phe Met Lys Arg Pro Ser Val Val Lys Asp Asn Cys Arg Arg 360 365 370	1220
cit atc gaa tcc atg cac aag atg gcc aac gcc cct cgt ttc tgg cca Leu Ile Glu Ser Met His Lys Met Ala Asn Ala Pro Arg Phe Trp Pro 375 380 385	1268
gag cct gag agt gag ccc ggc atc ttg ggt gac atc tgc aac caa ggc Glu Pro Glu Ser Glu Pro Gly Ile Leu Gly Asp Ile Cys Asn Gln Gly 390 395 400	1316
ctg tca cct gcc cca act ttc tgc aac cgc atg gac aca gca gtc gag Leu Ser Pro Ala Pro Thr Phe Cys Asn Arg Met Asp Thr Ala Val Glu 405 410 415 420	1364
acc cag cct aca tgc agg tca ccc tcc cac aag gtc cct gac ttg aag Thr Gln Pro Thr Cys Arg Ser Pro Ser His Lys Val Pro Asp Leu Lys 425 430 435	1412
aca tca gag gtt gag aag gcc agt ccc tgt cca tca cct ggc tct tgt Thr Ser Glu Val Glu Lys Ala Ser Pro Cys Pro Ser Pro Gly Ser Cys 440 445 450	1460
cac cca ccc aat agc agt ggg gcc cca gtg ctc atc aaa gcc agg tcc His Pro Pro Asn Ser Ser Gly Ala Pro Val Leu Ile Lys Ala Arg Ser 455 460 465	1508
ctg agc gtc cag cat gtg ccc agc tcc cag gaa gca gcc gag ggc agc	1556

16/22

Leu Ser Val Gln His Val Pro Ser Ser Gln Glu Ala Ala Glu Gly Ser			
470	475	480	
atc cgc tgc cgg tct cgg agt atc cag tac tgt gtt tcc caa gat gga			1604
Ile Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Ser Gln Asp Gly			
485	490	495	500
gct gct tcc ctg act gag aac aag ccc act ggc tcc cca gcc tcc ctg			1652
Ala Ala Ser Leu Thr Glu Ser Lys Pro Thr Gly Ser Pro Ala Ser Leu			
505	510	515	
aag acc cgt cca tcc cag ctt cca gtg tca gac cag acc tct cca tgc			1700
Lys Thr Arg Pro Ser Gln Leu Pro Val Ser Asp Gln Thr Ser Pro Cys			
520	525	530	
aaa tgc aca tgc aag gaa cca tct cct gtg tcc ccc atc act gtg ctc			1748
Lys Cys Thr Cys Lys Glu Pro Ser Pro Val Ser Pro Ile Thr Val Leu			
535	540	545	
aag gct gga ggc acc aaa gca cct ccc caa cac ctg ccc ctg tca cca			1796
Lys Ala Gly Gly Thr Lys Ala Pro Pro Gln His Leu Pro Leu Ser Pro			
550	555	560	
gcc ctg aca cgg gca gta gaa ggc gtc cag tac att gca gac cac ctc			1844
Ala Leu Thr Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp His Leu			
565	570	575	580
aag gca gaa gac aca gac ttc tcg gtg aag gag gac tgg aaa tac gtg			1892
Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val			
585	590	595	
gcc atg gtc att gac cga atc ttc ctc tgg atg ttc atc att gtc tgc			1940
Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile Val Cys			
600	605	610	
ctt ctg ggc act gtg gga ctc ttc ctg cct cca tgg ttg gct ggt atg			1988
Leu Leu Gly Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala Gly Met			
615	620	625	
atc tag ggaatagcgg cacctagctc ccaggctct acagggccat gcgactcgta			2044
Ile			
agtcacccac atcttccaaa ccggccatga gacacctagg agagagagat gctgccctgg			2104

17/22

ttgaccctgg ttctagtcag gccacaggcc tgggtggagc tagttgagga ctgatatagt	2164
tacaggctga gtccctcatt aaagtttctc cagagcaagt gacagtcact ccctggcita	2224
cagacagcac acacccatct gtgtcacaga gaatgatcca gtgttgatct cagttgtcct	2284
ttgaggccaa aacaattcat cccccttcag gaaccagagc ccctcggtct gtgggattcc	2344
tacggcccag gaaattccca tggtgctctg cggccacac ccctccctc cccataatgt	2404
ggitccctca accctccagg ctgggtgtct ctctgactca aaggtgtcag atgttaagccc	2464
cggcagggtt ttattttgtt taggttgaag cgaattggta agaaaatagag cagttagata	2524
tgtggatgag tcccactcac aggtgaatga gtgcagggtc tcacaggaag agtgagggcac	2584
cacaggactc ctgcttccat ctcagggtca caggcatcaa tcatgagcat ttccctagggt	2644
ccataaaaccc gaggagggca agggcataga gggtctcagg gtgtgtatgg agccaaatcc	2704
tgcaggggc ctgggccgtt catccctca tggatcttcc ttgatataccc tgtatgtttc	2764
tgcctctctg gaattagaag actgaaagta agatttcica tcacggtcct gtgggtgtggc	2824
cacagttcac ctgagcacat ctctctagac cagtaggagt gggtgcgaagc ccctcaatg	2884
tgttagaata gcgtgagctg ccaagagact tctaagcaaa acaggctctg tgactcattt	2944
ttcgagggcc atcgaccaag tcttaggggt gcctcacccct gtctgccttg cacttaggga	3004
agacccgaga gtttcccttt ccccttccca agatggcacc aggcaaccta gagaacccac	3064
cgtgggtggaa tgggagaacg aacatgtgt gcacatctt atgagattcc actgagtgaa	3124
gcccagaaca tgggaggcat gcaagaaatc accctgtgtc gtggtcccag ttgaccctcc	3184
gcgtctcca ccagccaggtt gggtttcaca gagctggcc ctgcacccctc agccaagctg	3244
ttcttagggcc tgaagctgag gtccctgttt ggatagtcct ggggactgca gaatgaaaga	3304
agaacttaat gaacgcacca agcctccagt aggtacggct gccacctccg tggtatgact	3364
tgcccataccc agctgaatga ggatgtcagg aaggaggtat gccagagggc cagcattgcc	3424
tttacctgac tacctacagg caaatccacc ttiaaacaca gagctgctgg acatccaggg	3484

18/22

tgctggtggg aaaggaactc cacactggga gccccaggcc attcctatga acaggaaggg	3544
gatgcagagg cctggtctct gaactctgga tattgttcca ggcttcctt agagtcctaa	3604
gggcattcgag gatcccatct gccatgtttc agtctgccct ccactgactg actagatctc	3664
tagccccat attgaaactg tcgggatgct gcaagatgac cctgggggg aaaticatgc	3724
cagaatctgg gaccaagggg aacacaagcc ccagtgtatga agacacgagg taacacctga	3784
cagaatgtgt ttctaccatt atgggtgcata cgtggctcca accacaagaa atgcagacaa	3844
cagtggagat cagggcaagg ccattgtgac atgaaacagg accgctgtgc tggctcttc	3904
agggttagga aaactgaact gctgggatgc tcctgacagg ctacccactt cccctaccc	3964
cccaacacac attcacaagc cagaaaagga aaataaaaca ccgtgttctc cccattccca	4024
ctcagccggc ctttgtctg cctgcttcca gtgttgatat gtgtcaaga taaagttcag	4084
ttagggcaga atgcttgatt taagactttt gaaccagtga gctttaaaga acagagactg	4144
tgtggccca gcccctctga tacgtagaca ttatctcccc aaagctccca gtcctccag	4204
tctaccccat cccatttagac agcatcaact caaatgttag tcttgagac cagttcggt	4264
agccatcata tgtctggaa tcccatattt gactctgcaa tgtctggctt cttcgcttg	4324
tgtggccaag gctcatctgc ggtgttgtgt gtgatagact cattgctgtt gtgtgcttgt	4384
tggatcttag ttgtttctgt ctgaataaac cgagtcgtgg tgtctcccc caaaaaaaaaa	4444
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	4504
aaaa	4508

<210> 5
 <211> 629
 <212> PRT
 <213> Mus musculus

<400> 5

19/22

Met Glu Ile Gly Gly Ser Gly Ala Pro Pro Pro Leu Leu Leu Pro
 1 5 10 15

Leu Leu Leu Leu Gly Thr Gly Leu Leu Pro Ala Ser Ser His Ile
 20 25 30

Glu Thr Arg Ala His Ala Glu Glu Arg Leu Leu Lys Arg Leu Phe Ser
 35 40 45

Gly Tyr Asn Lys Trp Ser Arg Pro Val Ala Asn Ile Ser Asp Val Val
 50 55 60

Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu
 65 70 75 80

Lys Asn Gln Met Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His
 85 90 95

Asp Tyr Lys Leu Arg Trp Asp Pro Gly Asp Tyr Glu Asn Val Thr Ser
 100 105 110

Ile Arg Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp Ile Val Leu Tyr
 115 120 125

Asn Asn Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His
 130 135 140

Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys
 145 150 155 160

Ser Ser Cys Ser Ile Asp Val Thr Phe Phe Pro Phe Asp Gln Gln Asn
 165 170 175

Cys Thr Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys Ile Asp

20/22

180

185

190

Leu Val Ser Met His Ser Arg Val Asp Gin Leu Asp Phe Trp Glu Ser
195 200 205

Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys
210 215 220

Tyr Glu Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Phe Ile
225 230 235 240

Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys
245 250 255

Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Glu
260 265 270

Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr
275 280 285

Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val
290 295 300

Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr
305 310 315 320

Leu Ser Ile Val Ile Thr Val Phe Val Leu Asn Val His His Arg Ser
325 330 335

Pro Arg Thr His Thr Met Pro Ala Trp Val Arg Arg Val Phe Leu Asp
340 345 350

Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Val Val Lys Asp
355 360 365

21/22

Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala Pro
370 375 380

Arg Phe Trp Pro Glu Pro Glu Ser Glu Pro Gly Ile Leu Gly Asp Ile
385 390 395 400

Cys Asn Gln Gly Leu Ser Pro Ala Pro Thr Phe Cys Asn Arg Met Asp
405 410 415

Thr Ala Val Glu Thr Gln Pro Thr Cys Arg Ser Pro Ser His Lys Val
420 425 430

Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala Ser Pro Cys Pro Ser
435 440 445

Pro Gly Ser Cys His Pro Pro Asn Ser Ser Gly Ala Pro Val Leu Ile
450 455 460

Lys Ala Arg Ser Leu Ser Val Gln His Val Pro Ser Ser Gln Glu Ala
465 470 475 480

Ala Glu Gly Ser Ile Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val
485 490 495

Ser Gln Asp Gly Ala Ala Ser Leu Thr Glu Ser Lys Pro Thr Gly Ser
500 505 510

Pro Ala Ser Leu Lys Thr Arg Pro Ser Gln Leu Pro Val Ser Asp Gln
515 520 525

Thr Ser Pro Cys Lys Cys Thr Cys Lys Glu Pro Ser Pro Val Ser Pro
530 535 540

22/22

Ile Thr Val Leu Lys Ala Gly Gly Thr Lys Ala Pro Pro Gln His Leu
545 550 555 560

Pro Leu Ser Pro Ala Leu Thr Arg Ala Val Glu Gly Val Gln Tyr Ile
565 570 575

Ala Asp His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu Asp
580 585 590

Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met Phe
595 600 605

Ile Ile Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro Pro Trp
610 615 620

Leu Ala Gly Met Ile
625

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

BLACK BORDERS

IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

FADED TEXT OR DRAWING

BLURRED OR ILLEGIBLE TEXT OR DRAWING

SKEWED/SLANTED IMAGES

COLOR OR BLACK AND WHITE PHOTOGRAPHS

GRAY SCALE DOCUMENTS

LINES OR MARKS ON ORIGINAL DOCUMENT

REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.